

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lau, Lester F.
- (ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
  - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
  - (C) CITY: Chicago
  - (D) STATE: Illinois
  - (E) COUNTRY: United States of America
  - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Clough, David W.
  - (B) REGISTRATION NUMBER: 36,107
  - (C) REFERENCE/DOCKET NUMBER: 28758/33766
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 312/474-6300
  - (B) TELEFAX: 312/474-0448
  - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1480 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 180..1316
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
  - (D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"

202210151500F



GAG Glu	TTA Leu	ATC Ile	GCA Ala	ATT Ile	GGA Gly	AAA Lys	GGC Gly	AGC Ser	TCA Ser	CTG Leu	AAG Lys	AGG Arg	CTT Leu	CCT Pro	GTC Val	803
195200205																
TTT Phe	GGC Gly	ACC Thr	GAA Glu	CCG Pro	CGA Arg	GTT Val	CTT Leu	TTC Phe	AAC Asn	CCT Pro	CTG Leu	CAC His	GCC Ala	CAT His	GGC Gly	851
210215220																
CAG Gln	AAA Lys	TGC Cys	ATC Ile	GTT Val	CAG Gln	ACC Thr	ACG Thr	TCT Ser	TGG Trp	TCC Ser	CAG Gln	TGC Cys	TCC Ser	AAG Lys	AGC Ser	899
225230235240																
TGC Cys	GGA Gly	ACT Thr	GGC Gly	ATC Ile	TCC Ser	ACA Thr	CGA Arg	GTT Val	ACC Thr	AAT Asn	GAC Asp	AAC Asn	CCA Pro	GAG Glu	TGC Cys	947
245250255																
CGC Arg	CTG Leu	GTG Val	AAA Lys	GAG Glu	ACC Thr	CGG Arg	ATC Ile	TGT Cys	GAA Glu	GTG Val	CGT Arg	CCT Pro	TGT Cys	GGA Gly	CAA Gln	995
260265270																
CCA Pro	GTG Val	TAC Tyr	AGC Ser	AGC Ser	CTA Leu	AAA Lys	AAG Lys	GGC Gly	AAG Lys	AAA Lys	TGC Cys	AGC Ser	AAG Lys	ACC Thr	AAG Lys	1043
275280285																
AAA Lys	TCC Ser	CCA Pro	GAA Glu	CCA Pro	GTC Val	AGA Arg	TTT Phe	ACT Thr	TAT Tyr	GCA Ala	GGA Gly	TGC Cys	TCC Ser	AGT Ser	GTC Val	1091
290295300																
AAG Lys	AAA Lys	TAC Tyr	CGG Arg	CCC Pro	AAA Lys	TAC Tyr	TGC Cys	GGC Gly	TCC Ser	TGC Cys	GTA Val	GAT Asp	GGC Gly	CGG Arg	TGC Cys	1139
305310315320																
TGC Cys	ACA Thr	CCT Pro	CTG Leu	CAG Gln	ACC Thr	AGA Arg	ACT Thr	GTG Val	AAG Lys	ATG Met	CGG Arg	TTC Phe	CGA Arg	TGC Cys	GAA Glu	1187
325330335																
GAT Asp	GGA Gly	GAG Glu	ATG Met	TTT Phe	TCC Ser	AAG Lys	AAT Asn	GTC Val	ATG Met	ATG Met	ATC Ile	CAG Gln	TCC Ser	TGC Cys	AAA Lys	1235
340345350																
TGT Cys	AAC Asn	TAC Tyr	AAC Asn	TGC Cys	CCG Pro	CAT His	CCC Pro	AAC Asn	GAG Glu	GCA Ala	TCG Ser	TTC Phe	CGA Arg	CTG Leu	TAC Tyr	1283
355360365																
AGC Ser	CTA Leu	TTC Phe	AAT Asn	GAC Asp	ATC Ile	CAC His	AAG Lys	TTC Phe	AGG Arg	GAC Asp	TAAGTGCCTC	CAGGGTTCCT				1336
370375																
AGTGTGGGCT GGACAGAGGA GAAGCGCAAG CATCATGGAG ACGTGGGTGG GCGGAGGATG																1396
AATGGTGCCT TGCTCATTCT TGAGTAGCAT TAGGGTATTT CAAAACTGCC AAGGGGCTGA																1456
TGTGGACGGA CAGCAGCGCA GCCG																1480

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu  
1 5 10 15  
His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys  
20 25 30  
Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp  
35 40 45  
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
50 55 60  
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
65 70 75 80  
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu  
85 90 95  
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser  
100 105 110  
Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val  
115 120 125  
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly  
130 135 140  
Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu  
145 150 155 160  
Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp  
165 170 175  
Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn  
180 185 190  
Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val  
195 200 205  
Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly  
210 215 220  
Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser  
225 230 235 240

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys  
245 250 255

Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln  
260 265 270

Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys  
275 280 285

Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val  
290 295 300

Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys  
305 310 315 320

Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu  
325 330 335

Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys  
340 345 350

Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr  
355 360 365

Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp  
370 375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..1266

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCGGGCCC ACCGCGACAC CGCGCCGCCA CCCCACCC GCTGCGCACG GCCTGTCCGC	60
TGCACACCAG CTTGTTGGCG TCTTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC	120
ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT	168
Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu	
1 5 10 15	
CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC	216
Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His	

2003-07-25 15:00

20							25						30					
TGC	CCC	CTG	GAG	GCG	CCC	AAG	TGC	GCG	CCG	GGA	GTC	GGG	CTG	GTC	CGG	264		
Cys	Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg			
			35				40						45					
GAC	GGC	TGC	GGC	TGC	TGT	AAG	GTC	TGC	GCC	AAG	CAG	CTC	AAC	GAG	GAC	312		
Asp	Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp			
			50				55						60					
TGC	AGC	AAA	ACG	CAG	CCC	TGC	GAC	CAC	ACC	AAG	GGG	CTG	GAA	TGC	AAC	360		
Cys	Ser	Lys	Thr	Gln	Pro	Cys	Asp	His	Thr	Lys	Gly	Leu	Glu	Cys	Asn			
		65				70						75						
TTC	GGC	GCC	AGC	TCC	ACC	GCT	CTG	AAG	GGG	ATC	TGC	AGA	GCT	CAG	TCA	408		
Phe	Gly	Ala	Ser	Ser	Thr	Ala	Leu	Lys	Gly	Ile	Cys	Arg	Ala	Gln	Ser			
80					85						90			95				
GAG	GGC	AGA	CCC	TGT	GAA	TAT	AAC	TCC	AGA	ATC	TAC	CAA	AAC	GGG	GAA	456		
Glu	Gly	Arg	Pro	Cys	Glu	Tyr	Asn	Ser	Arg	Ile	Tyr	Gln	Asn	Gly	Glu			
			100						105			110						
AGT	TTC	CAG	CCC	AAC	TGT	CAA	CAT	CAG	TGC	ACA	TGT	ATT	GAT	GGC	GCC	504		
Ser	Phe	Gln	Pro	Asn	Cys	Gln	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala			
			115						120			125						
GTG	GGC	TGC	ATT	CCT	CTG	TGT	CCC	CAA	GAA	CTA	TCT	CTC	CCC	AAC	TTG	552		
Val	Gly	Cys	Ile	Pro	Leu	Cys	Pro	Gln	Glu	Leu	Ser	Leu	Pro	Asn	Leu			
		130						135						140				
GGC	TGT	CCC	AAC	CCT	CGG	CTG	GTC	AAA	GTT	ACC	GGG	CAG	TGC	TGC	GAG	600		
Gly	Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys	Val	Thr	Gly	Gln	Cys	Cys	Glu			
		145						150						155				
GAG	TGG	GTC	TGT	GAC	GAG	GAT	AGT	ATC	AAG	GAC	CCC	ATG	GAG	GAC	CAG	648		
Glu	Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile	Lys	Asp	Pro	Met	Glu	Asp	Gln			
160					165						170			175				
GAC	GGC	CTC	CTT	GGC	AAG	GAG	CTG	GGA	TTC	GAT	GCC	TCC	GAG	GTG	GAG	696		
Asp	Gly	Leu	Leu	Gly	Lys	Glu	Leu	Gly	Phe	Asp	Ala	Ser	Glu	Val	Glu			
			180						185			190						
TTG	ACG	AGA	AAC	AAT	GAA	TTG	ATT	GCA	GTT	GGA	AAA	GGC	AGA	TCA	CTG	744		
Leu	Thr	Arg	Asn	Asn	Glu	Leu	Ile	Ala	Val	Gly	Lys	Gly	Arg	Ser	Leu			
			195						200			205						
AAG	CGG	CTC	CCT	GTT	TTT	GGA	ATG	GAG	CCT	CGC	ATC	CTA	TAC	AAC	CCT	792		
Lys	Arg	Leu	Pro	Val	Phe	Gly	Met	Glu	Pro	Arg	Ile	Leu	Tyr	Asn	Pro			
		210						215						220				
TTA	CAA	GGC	CAG	AAA	TGT	ATT	GTT	CAA	ACA	ACT	TCA	TGG	TCC	CAG	TGC	840		
Leu	Gln	Gly	Gln	Lys	Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys			
		225						230						235				
TCA	AAG	ACC	TGT	GGA	ACT	GGT	ATC	TCC	ACA	CGA	GTT	ACC	AAT	GAC	AAC	888		
Ser	Lys	Thr	Cys	Gly	Thr	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn			
240					245						250			255				

CCT GAG TGC CGC CTT GTG AAA GAA ACC CGG ATT TGT GAG GTG CGG CCT 936  
 Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro  
 260 265 270

TGT GGA CAG CCA GTG TAC AGC AGC CTG AAA AAG GGC AAG AAA TGC AGC 984  
 Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser  
 275 280 285

AAG ACC AAG AAA TCC CCC GAA CCA GTC AGG TTT ACT TAC GCT GGA TGT 1032  
 Lys Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys  
 290 295 300

TTG AGT GTG AAG AAA TAC CGG CCC AAG TAC TGC GGT TCC TGC GTG GAC 1080  
 Leu Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp  
 305 310 315

GGC CGA TGC TGC ACG CCC CAG CTG ACC AGG ACT GTG AAG ATG CGG TTC 1128  
 Gly Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe  
 320 325 330 335

CGC TGC GAA GAT GGG GAG ACA TTT TCC AAG AAC GTC ATG ATG ATC CAG 1176  
 Arg Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln  
 340 345 350

TCC TGC AAA TGC AAC TAC AAC TGC CCG CAT GCC AAT GAA GCA GCG TTT 1224  
 Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe  
 355 360 365

CCC TTC TAC AGG CTG TTC AAT GAC ATT CAC AAA TTT AGG GAC 1266  
 Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp  
 370 375 380

TAAATGCTAC CTGGGTTTCC AGGGCACACC TAGACAAACA AGGGAGAAGA GTGTCAGAAT 1326

CAGAATCATG GAGAAAATGG GCGGGGGTGG TGTGGGTGAT GGGACTCATT GTAGAAAGGA 1386

AGCCTTCTCA TTCTTGAGGA GCATTAAGGT AT 1418

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "Human Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu  
 1 5 10 15

His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys  
20 25 30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp  
35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
50 55 60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
65 70 75 80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu  
85 90 95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser  
100 105 110

Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala Val  
115 120 125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly  
130 135 140

Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu  
145 150 155 160

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp  
165 170 175

Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu  
180 185 190

Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu Lys  
195 200 205

Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu  
210 215 220

Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser  
225 230 235 240

Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro  
245 250 255

Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys  
260 265 270

Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys  
275 280 285

Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu  
290 295 300

Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly  
305 310 315 320

1007-ES-001



Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg  
325 330 335

Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser  
340 345 350

Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro  
355 360 365

Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp  
370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "Fisp12 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGCC	GACAACCCCA	GACGCCACCG	CCTGGAGCGT	CCAGACACCA	ACCTCCGCCC	60
CTGTCCGAAT	CCAGGCTCCA	GCCGCGCCTC	TCGTGCGCTC	TGCACCCTGC	TGTGCATCCT	120
CCTACCGCGT	CCCGATCATG	CTCGCCTCCG	TCGCAGGTCC	CATCAGCCTC	GCCTTGGTGC	180
TCCTCGCCCT	CTGCACCCGG	CCTGCTACGG	GCCAGGACTG	CAGCGCGCAA	TGTCAGTGCG	240
CAGCCGAAGC	AGCGCCGCAC	TGCCCCGCCG	GCGTGAGCCT	GGTGCTGGAC	GGCTGCGGCT	300
GCTGCCGCGT	CTGCGCCAAG	CAGCTGGGAG	AACTGTGTAC	GGAGCGTGAC	CCCTGCGACC	360
CACACAAGGG	CCTCTTCTGC	GATTTCGGCT	CCCCCGCCAA	CCGCAAGATT	GGAGTGTGCA	420
CTGCCAAAGA	TGGTGACCCC	TGTGTCTTCG	GTGGGTCGGT	GTACCGCAGC	GGTGAGTCCT	480
TCCAAAGCAG	CTGCAAATAC	CAATGCACTT	GCCTGGATGG	GGCCGTGGGC	TGCGTGCCCC	540
TATGCAGCAT	GGACGTGCGC	CTGCCCAGCC	CTGACTGCCC	CTTCCCGAGA	AGGGTCAAGC	600
TGCCTGGGAA	ATGCTGCAAG	GAGTGGGTGT	GTGACGAGCC	CAAGGACCGC	ACAGCAGTTG	660
GCCCTGCCCT	AGCTGCCTAC	CGACTGGAAG	ACACATTTGG	CCCAGACCCA	ACTATGATGC	720
GAGCCAACTG	CCTGGTCCAG	ACCACAGAGT	GGAGCGCCTG	TTCTAAGACC	TGTGGAATGG	780
GCATCTCCAC	CCGAGTTACC	AATGACAATA	CCTTCTGCAG	ACTGGAGAAG	CAGAGCCGCC	840
TCTGCATGGT	CAGGCCCTGC	GAAGCTGACC	TGGAGGAAAA	CATTAAGAAG	GGCAAAAAGT	900

20221010 15:50:01

GCATCCGGAC	ACCTAAAATC	GCCAAGCCTG	TCAAGTTTGA	GCTTTCTGGC	TGCACCAGTG	960
TGAAGACATA	CAGGGCTAAG	TTCTGCGGGG	TGTGCACAGA	CGGCCGCTGC	TGCACACCGC	1020
ACAGAACCAC	CACTCTGCCA	GTGGAGTTCA	AATGCCCCGA	TGGCGAGATC	ATGAAAAAGA	1080
ATATGATGTT	CATCAAGACC	TGTGCCTGCC	ATTACAACTG	TCCTGGGGAC	AATGACATCT	1140
TTGAGTCCCT	GTACTACAGG	AAGATGTACG	GAGACATGGC	GTAAAGCCAG	GAAGTAAGGG	1200
ACACGAACTC	ATTAGACTAT	AACTTGAACT	GAGTTGCATC	TCATTTTCTT	CTGTAAAAAC	1260
AATTACAGTA	GCACATTAAT	TTAAATCTGT	GTTTTTAACT	ACCGTGGGAG	GAAGTATCCC	1320
ACCAAAGTGA	GAACGTTATG	TCATGGCCAT	ACAAGTAGTC	TGTCAACCTC	AGACACTGGT	1380
TTCGAGACAG	TTTACACTTG	ACAGTTGTTC	ATTAGCGCAC	AGTGCCAGAA	CGCACACTGA	1440
GGTGAGTCTC	CTGGAACAGT	GGAGATGCCA	GGAGAAAAGAA	AGACAGGTAC	TAGCTGAGGT	1500
TATTTTAAAA	GCAGCAGTGT	GCCTACTTTT	TGGAGTGTA	CCGGGGAGGG	AAATTATAGC	1560
ATGCTTGCAG	ACAGACCTGC	TCTAGCGAGA	GCTGAGCATG	TGTCCTCCAC	TAGATGAGGC	1620
TGAGTCCAGC	TGTTCTTTAA	GAACAGCAGT	TTCAGCCTCT	GACCATTCTG	ATTCCAGTGA	1680
CACTTGTGAG	GAGTCAGAGC	CTTGTCTGTT	AGACTGGACA	GCTTGTGGCA	AGTAAGTTTG	1740
CCTGTAACAA	GCCAGATTTT	TATTGATATT	GTAAATATTG	TGGATATATA	TATATATATA	1800
TATATTTGTA	CAGTTATCTA	AGTTAATTTA	AAGTCATTTG	TTTTTGTTTT	AAGTGCTTTT	1860
GGGATTTTAA	ACTGATAGCC	TCAAACCTCA	AACACCATAG	GTAGGACACG	AAGCTTATCT	1920
GTGATTCAAA	ACAAAGGAGA	TACTGCAGTG	GGAATTGTGA	CCTGAGTGAC	TCTCTGTCAG	1980
AACAAACAAA	TGCTGTGCAG	GTGATAAAGC	TATGTATTGG	AAGTCAGATT	TCTAGTAGGA	2040
AATGTGGTCA	AATCCCTGTT	GGTGAACAAA	TGGCCTTTAT	TAAGAAATGG	CTGGCTCAGG	2100
GTAAGGTCCG	ATTCCTACCA	GGAAGTGCTT	GCTGCTTCTT	TGATTATGAC	TGGTTTGGGG	2160
TGGGGGGCAG	TTTATTTGTT	GAGAGTGTGA	CCAAAAGTTA	CATGTTTGCA	CCTTTCTAGT	2220
TGAAAATAAA	GTATATATAT	ATTTTTTATA	TGAAAAAATA	GGAATTC		2267

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(D) OTHER INFORMATION: "Fispl2 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu Ala Leu Val Leu Leu  
1 5 10 15  
Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys  
20 25 30  
Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro Ala Gly Val Ser Leu  
35 40 45  
Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly  
50 55 60  
Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe  
65 70 75 80  
Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala  
85 90 95  
Lys Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly  
100 105 110  
Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly  
115 120 125  
Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser  
130 135 140  
Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys  
145 150 155 160  
Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro  
165 170 175  
Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr  
180 185 190  
Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys  
195 200 205  
Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn  
210 215 220  
Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro  
225 230 235 240  
Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile  
245 250 255  
Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys  
260 265 270

20250303 012200

Thr Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp  
275 280 285

Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe  
290 295 300

Lys Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys  
305 310 315 320

Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu  
325 330 335

Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
340 345

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: "CTGF cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG 60  
CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA 120  
GTGCCAACCA TGACCGCCGC CAGTATGGGC CCCGTCCGCG TCGCCTTCGT GGTCTCCTC 180  
GCCCTCTGCA GCCGGCCGGC CGTCGGCCAG AACTGCAGCG GGCCGTGCCG GTGCCCCGAC 240  
GAGCCGGCGC CGCGCTGCCC GGCGGGCGTG AGCCTCGTGC TGGACGGCTG CGGCTGCTGC 300  
CGCGTCTGCG CCAAGCAGCT GGGCGAGCTG TGCACCGAGC GCGACCCCTG CGACCCGCAC 360  
AAGGGCCTCT TCTGTGACTT CGGCTCCCCG GCCAACCGCA AGATCGGCGT GTGCACCGCC 420  
AAAGATGGTG CTCCCTGCAT CTTCGGTGGT ACGGTGTACC GCAGCGGAGA GTCCTTCCAG 480  
AGCAGCTGCA AGTACCAGTG CACGTGCCTG GACGGGGCGG TGGGCTGCAT GCCCCTGTGC 540  
AGCATGGACG TTCGTCTGCC CAGCCCTGAC TGCCCCCTCC CGAGGAGGGT CAAGCTGCCC 600  
GGGAAATGCT GCGAGGAGTG GGTGTGTGAC GAGCCCAAGG ACCAAACCGT GGTGGGCCT 660  
GCCCTCGCGG CTTACCGACT GGAAGACACG TTTGGCCCAG ACCCAACTAT GATTAGAGCC 720  
AACTGCCTGG TCCAGACCAC AGAGTGGAGC GCCTGTTCCA AGACCTGTGG GATGGGCATC 780

TCCACCCGGG TTACCAATGA CAACGCCTCC TGCAGGCTAG AGAAGCAGAG CCGCCTGTGC	840
ATGGTCAGGC CTTGCGAAGC TGACCTGGAA GAGAACATTA AGAAGGGCAA AAAGTGCATC	900
CGTACTCCCA AAATCTCCAA GCCTATCAAG TTTGAGCTTT CTGGCTGCAC CAGCATGAAG	960
ACATACCGAG CTAAATTCTG TGGAGTATGT ACCGACGGCC GATGCTGCAC CCCCCACAGA	1020
ACCACCACCC TGCCGGTGGA GTTCAAGTGC CCTGACGGCG AGGTCATGAA GAAGAACATG	1080
ATGTTTCATCA AGACCTGTGC CTGCCATTAC AACTGTCCCG GAGACAATGA CATCTTTGAA	1140
TCGCTGTACT ACAGGAAGAT GTACGGAGAC ATGGCATGAA GCCAGAGAGT GAGAGACATT	1200
AACTCATTAG ACTGGAAGTT GAAGTGATTC ACATCTCATT TTTCCGTAAA AATGATTTCA	1260
GTAGCACAAG TTATTTAAAT CTGTTTTTCT AACTGGGGGA AAAGATTCCC ACCCAATTCA	1320
AAACATTGTG CCATGTCAAA CAAATAGTCT ATCTTCCCCA GACACTGGTT TGAAGAATGT	1380
TAAGACTTGA CAGTGGAAGT ACATTAGTAC ACAGCACCAG AATGTATATT AAGGTGTGGC	1440
TTTAGGAGCA GTGGGAGGGT ACCGGCCCCG TTAGTATCAT CAGATCGACT CTTATACGAG	1500
TAATATGCCT GCTATTTGAA GTGTAATTGA GAAGGAAAAT TTTAGCGTGC TCACTGACCT	1560
GCCTGTAGCC CCAGTGACAG CTAGGATGTG CATTCTCCAG CCATCAAGAG ACTGAGTCAA	1620
GTTGTTCCCTT AAGTCAGAAC AGCAGACTCA GCTCTGACAT TCTGATTCGA ATGACACTGT	1680
TCAGGAATCG GAATCCTGTC GATTAGACTG GACAGCTTGT GGCAAGTGAA TTTGCCTGTA	1740
ACAAGCCAGA TTTTTTAAAA TTTATATTGT AAATATTGTG TGTGTGTGTG TGTGTGTATA	1800
TATATATATA TATGTACAGT TATCTAAGTT AATTTAAAGT TGTTTGTGCC TTTTTATTTT	1860
TGTTTTTAAT GCTTTGATAT TTCAATGTTA GCCTCAATTT CTGAACACCA TAGGTAGAAT	1920
GTAAAGCTTG TCTGATCGTT CAAAGCATGA AATGGATACT TATATGGAAA TTCTGCTCAG	1980
ATAGAATGAC AGTCCGTCAA AACAGATTGT TTGCAAAGGG GAGGCATCAG TGTCTTGCCA	2040
GGCTGATTTT TAGGTAGGAA ATGTGGTAGC TCACG	2075

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "CTGF amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu  
1 5 10 15

Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro  
20 25 30

Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser  
35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu  
50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu  
65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr  
85 90 95

Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser  
100 105 110

Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp  
115 120 125

Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro  
130 135 140

Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys  
145 150 155 160

Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly  
165 170 175

Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro  
180 185 190

Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala  
195 200 205

Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp  
210 215 220

Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg  
225 230 235 240

Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys  
245 250 255

Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly  
260 265 270

Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr  
275 280 285

005753-01220

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu  
290 295 300

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile  
305 310 315 320

Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe  
325 330 335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
340 345

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGATCTGT GACGAGCCCA AGGAC

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGAATTCGA CCAGGCAGTT GGCTCG

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

2022-03-03 10:00:00

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGATCCTG TGATGAAGAC AGCATT

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAATTCAA CGATGCATTT CTGGCC

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp  
1 5 10 15

Cys Ser Lys Thr Gln  
20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

202310-09-04



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys  
1 5 10 15

Ile Pro Leu Cys Pro  
20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser Cys Gly  
1 5 10 15

Thr Gly Ile Ser Thr Arg Val Thr  
20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys  
1 5 10 15

Glu Thr Arg Ile Cys Glu Val Arg Pro Cys  
20 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant

20250705 15:40:00

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	Arg	Cys	Cys	Thr	Pro	Leu	Gln
1				5					10					15	

Thr	Arg	Thr	Val	Lys
			20	

20251010 10:54:50